



## FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
GGAGGGGAGGCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG  
GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG  
CTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG  
ACAACATGATGGTCAAGAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT  
TCAAAGGGTGCTGGCTGAACCGGTCAAGTATTATTTTTCGCGGAGGTGATAAGTGGTCAGT  
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTCACTCAACATACACCCAGAACA  
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA  
TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTGAAAATGGACAATATTTGGACATT  
TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAATGCTGTGTCTATT  
CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTCAGGAAATTAAAT  
CTGGCACCGTGACCCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT  
TCAAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA  
ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCT  
CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT  
TGTGTTGACACTGTCTCTTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA  
TTCAAAGACCCATAAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC  
TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTTGATTAGCTACATTA  
CCTTGTGAAGCAGTACACATTGTCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG  
AGGATATTAATTGTGATTTCATGTTTGTAACTTACAACCTTTCAAAGCATTTCAGTCATGGT  
CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA  
GGCTGCAATACAAGCATTTCAGTTCCTGTTTTCAATAAGAGTCAATCCACATTTACAAAGATG  
CATTTTTTTCTTTTTTTGATAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA  
TAACACATATCTAGATTTTCTGCTTGCATGATATTTCAGGTTTCAGGAATGAGCCTTGTAAT  
ATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAAGTTCAGCATGGGTGTGCCTTCATAC  
AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTTGCTAAATCTTACAATTTGA  
AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACTATCTCTAAGTAACGAAGGAGC  
TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT  
AACTCAGTTCCTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCT  
TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCTTTTAAATGACAGCACA  
GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAAA  
TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCTTATCACCTAATATTACAAGAGTTGGTA  
AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA  
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA  
CAAGGAATAATTTCTGATCCAGGATCGTCCTTCAAATGGCTGTATTTATAAAGGTTTTTGG  
AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATGACCTGCCA  
AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA  
AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSII FAGGDKWSVDPRVSI STL NKR DYS LQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSF PDVRKV KVVVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILT VTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVL FSCWYLVLTLSSFTSIFYLKNAILQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 326-345

**N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

**Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

**Tyrosine kinase phosphorylation site.**

amino acids 178-186

**N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

**Myelin P0 protein:**

amino acids 92-121